Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

In the Claims

Claim 1 (original): A method for destabilizing non-specific duplex formation between a homopolymeric sequence of an oligonucleotide and a non-homopolymeric target nucleic acid, comprising a modification of said homopolymeric sequence of said oligonuclotide, wherein said modification decreases or abrogates hydrogen bonding between said modified oligonucleotide and a non-homopolymeric target sequence.

Claim 2 (original): The method of claim 1, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

Claim 3 (original): The method of claim 2, wherein said universal base is 3-nitropyrrole.

Claim 4 (previously presented): The method of claim 1, wherein said oligonucleotide is a homopolymer comprising at least one nucleotide modification.

Claim 5 (previously presented): The method of claim 1, wherein said oligonucleotide is a modified oligo d(T) homopolymer which comprises a modification which decreases or abrogates hydrogen bonding between said modified oligo d(T) homopolymer and a non-homopolymeric target sequence, and wherein said method is used during first strand synthesis, when preparing a cDNA library, such that said decrease or abrogation of bonding between said modified oligo d(T) homopolymer and said non-homopolymeric target sequence increases the proportion of full length cDNA clones in said library.

Claim 6 (original): The method of claim 5, wherein said modification is at least one universal base incorporated into said oligo d(T) homopolymer.

Claim 7 (original): The method of claim 6, wherein said universal base is 3-nitropyrrole.

Claim 8 (original): The method of claim 5, wherein said modification is at least one chemically modified nucleoside incorporated into said oligo d(T) homopolymer.

Claim 9 (original): The method of claim 5, wherein said modification is at least one base analog incorporated into said oligo d(T) homopolymer.

Claim 10 (original): The method of claim 9, wherein said base analog is inosine.

Claim 11 (original): The method of claim 5, wherein said modification is at least one mismatch incorporated into said oligo d(T) homopolymer.

Claim 12 (original): The method of claim 5, wherein said modification is a phosphate or ribose modification incorporated into said oligo d(T) homopolymer.

Claim 13 (previously presented): The method according to claim 5, wherein an enzyme capable of RNA-dependent DNA polymerization is used for said first strand synthesis.

Claim 14 (previously presented): The method according to claim 13, wherein said enzyme is a reverse transcriptase selected from the group consisting of avian myoblastoid virus reverse transcriptase, murine moloney leukemia virus reverse transcriptase, and human immuno deficiency virus reverse transcriptase.

Claim 15 (previously presented): A kit for destabilizing non-specific duplex formation between a homopolymeric sequence of an oligonucleotide and a non-homopolymeric target nucleic acid, said kit comprising a modified homopolymeric oligonucleotide, wherein said modified oligonucleotide includes a modification which decreases or abrogates hydrogen bonding between said modified oligonucleotide and a non-homopolymeric target sequence.

Claim 16 (previously presented): The method of claim 1, wherein said oligonucleotide is a modified oligonucleotide primer which comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between said modified oligonucleotide primer and a non-homopolymeric target sequence, and wherein said method is used for reducing mispriming events during DNA synthesis, such that said decrease or abrogation of bonding between said modified oligonucleotide primer and said non-homopolymeric target sequence reduces mispriming events, while maintaining a formation of a duplex with a homopolymeric target sequence.

Claim 17 (previously presented): The method of claim 16, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

Claim 18 (previously presented): The method of claim 17, wherein said universal base is 3-nitropyrrole.

Claim 19 (previously presented): The method of claim 16, wherein said oligonucleotide is a homopolymer.

Claim 20 (previously presented): The method of claim 16, wherein said modified oligonucleotide primer is used for reducing mispriming during 5' RACE, thereby reducing mispriming events while maintaining a formation of a duplex with a homopolymeric target sequence, during 5' RACE.

Claim 21 (previously presented): The method of claim 20, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

Claim 22 (previously presented): The method of claim 20, wherein said universal base is 3-nitropyrrole.

Claim 23 (previously presented): The method of claim 22, wherein said modification is at least one chemically modified nucleoside incorporated into said homopolymeric sequence.

Claim 24 (previously presented): The method of claim 20, wherein said modification is at least one base analog incorporated into said homopolymeric sequence.

Claim 25 (previously presented): The method of claim 24, wherein said base analog is inosine.

Claim 26 (previously presented): The method of claim 20, wherein said modification is at least one mismatch incorporated into said homopolymeric sequence.

Claim 27 (previously presented): The method of claim 20, wherein said modification is a phosphate or ribose modification incorporated into said homopolymeric sequence.

Claim 28 (previously presented): The kit of claim 15, wherein said modified homopolymeric oligonucleotide is a primer for 5' RACE.

Claim 29 (previously presented): The method of claim 16, wherein said modified oligonucleotide primer is used for reducing mispriming during 3' RACE comprising a priming of said 3' RACE, thereby reducing mispriming events while maintaining a formation of a duplex with a homopolymeric target sequence, during 3' RACE.

Claim 30 (previously presented): The method of claim 29, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

Claim 31 (previously presented): The method of claim 16, wherein said modified oligonucleotide primer used for generating *bona fide* genetic markers, thereby reducing mispriming events from a non-homopolymeric target sequence while maintaining a formation of a duplex with a homopolymeric target sequence, and thereby generating *bona fide* genetic markers.

Claim 32 (previously presented): The method of claim 31, wherein said modified oligonucleotide primer primes from an internal A-rich region in an Alu repeat.

Clam 33 (previously presented): A method for stabilizing duplex formation between an oligonucleotide comprising a homopolymeric sequence and a target homopolymeric sequence comprising a modification of said homopolymeric sequence of said oligonucleotide, wherein said modification decreases or abrogates hydrogen bonding between said oligonucleotide and a non-homopolymeric target sequence, thereby stabilizing duplex formation between said oligonucleotide and said target homopolymeric sequence.

Claim 34 (previously presented): The method of claim 16, wherein said modified oligonucleotide primer is used for sequencing.

Claim 35 (cancelled)

Claim 36 (previously presented): The method of claim 5, further comprising a use of a second modified oligonucleotide during second strand synthesis from a 3' end-tailed first strand product, wherein said second modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between said second modified oligonucleotide and a second non-homopolymeric target sequence, thereby further increasing the proportion of full length cDNA clones in said library.

Claim 37 (previously presented): The kit of claim 15, wherein said modified homopolymeric oligonucleotide is an oligonucleotide d(T) homopolymeric primer, wherein said modified oligo d(T) homopolymeric primer decreases or abrogates hydrogen bonding between said modified oligo d(T) homopolymeric primer and a non-polyA target sequence, thereby improving the synthesis of cDNAs.